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RAW SEQUENCE LISTING

DATE: 04/10/2002

PATENT APPLICATION: US/10/025,676

TIME: 15:34:43

Input Set : N:\Crf3\RULE60\10025676.raw

Output Set: N:\CRF3\04102002\J025676.raw

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1 <110> APPLICANT: GUTIERREZ-ARMENTA, CRISANTO
2     SANZ-BURGOS, ANDRES P.
3     XIE, QI
4     LOPEZ, PAULA S.
5 <120> TITLE OF INVENTION: PLANT RETINOBLASTOMA-ASSOCIATED PROTEINS
6 <130> FILE REFERENCE: 604-468
7 <140> CURRENT APPLICATION NUMBER: 10/025,676
8 <141> CURRENT FILING DATE: 2001-12-26
10 <150> PRIOR APPLICATION NUMBER: 09/213,294
11 <151> PRIOR FILING DATE: 1998-12-14
14 <150> PRIOR APPLICATION NUMBER: PCT/ES96/00130
15 <151> PRIOR FILING DATE: 1996-06-13
16 <150> PRIOR APPLICATION NUMBER: PCT/EP97/03070
17 <151> PRIOR FILING DATE: 1997-06-12
18 <160> NUMBER OF SEQ ID NOS: 19
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 683
23 <212> TYPE: PRT
24 <213> ORGANISM: Unknown Organism
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Description of Unknown Organism: plant RB protein
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30     Ser Asn Ser Cys Lys Gly Glu Leu Asp Phe Lys Ser Ile Leu Ile Asn
31         20             25             30
32     Asn Asp Tyr Ile Pro Tyr Asp Glu Asn Ser Thr Gly Asp Ser Thr Asn
33         35             40             45
34     Leu Gly His Ser Lys Cys Ala Phe Glu Thr Leu Ala Ser Pro Thr Lys
35         50             55             60
36     Thr Ile Lys Asn Met Leu Thr Val Pro Ser Ser Pro Leu Ser Pro Ala
37         65             70             75             80
38     Thr Gly Gly Ser Val Lys Ile Val Gln Met Thr Pro Val Thr Ser Ala
39         85             90             95
40     Met Thr Thr Ala Lys Trp Leu Arg Glu Val Ile Ser Ser Leu Pro Asp
41         100            105            110
42     Lys Pro Ser Ser Lys Leu Gln Gln Phe Leu Ser Ser Cys Asp Arg Asp
43         115            120            125
44     Leu Thr Asn Ala Val Thr Glu Arg Val Ser Ile Val Leu Glu Ala Ile
45         130            135            140
46     Phe Pro Thr Lys Ser Ser Ala Asn Arg Gly Val Ser Leu Gly Leu Asn
47         145            150            155            160

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48   Cys Ala Asn Ala Phe Asp Ile Pro Trp Ala Glu Ala Arg Lys Val Glu
49           165                      170                      175
50   Ala Ser Lys Leu Tyr Tyr Arg Val Leu Glu Ala Ile Cys Arg Ala Glu
51           180                      185                      190
52   Leu Gln Asn Ser Asn Val Asn Asn Leu Thr Pro Leu Leu Ser Asn Glu
53           195                      200                      205
54   Arg Phe His Arg Cys Leu Ile Ala Cys Ser Ala Asp Leu Val Leu Ala
55           210                      215                      220
56   Thr His Lys Thr Val Ile Met Met Phe Pro Ala Val Leu Glu Ser Thr
57   225                      230                      235                      240
58   Gly Leu Thr Ala Phe Asp Leu Ser Lys Ile Ile Glu Asn Phe Val Arg
59           245                      250                      255
60   His Glu Glu Thr Leu Pro Arg Glu Leu Lys Arg His Leu Asn Ser Leu
61           260                      265                      270
62   Glu Glu Gln Leu Leu Glu Ser Met Ala Trp Glu Lys Gly Ser Ser Leu
63           275                      280                      285
64   Tyr Asn Ser Leu Ile Val Ala Arg Pro Ser Val Ala Ser Glu Ile Asn
65           290                      295                      300
66   Arg Leu Gly Leu Leu Ala Glu Pro Met Pro Ser Leu Asp Asp Leu Val
67   305                      310                      315                      320
68   Ser Arg Gln Asn Val Arg Ile Glu Gly Leu Pro Ala Thr Pro Ser Lys
69           325                      330                      335
70   Lys Arg Ala Ala Gly Pro Asp Asp Asn Ala Asp Pro Arg Ser Pro Lys
71           340                      345                      350
72   Arg Ser Cys Asn Glu Ser Arg Asn Thr Val Val Glu Arg Asn Leu Gln
73           355                      360                      365
74   Thr Pro Pro Pro Lys Gln Ser His Met Val Ser Thr Ser Leu Lys Ala
75           370                      375                      380
76   Lys Cys His Pro Leu Gln Ser Thr Phe Ala Ser Pro Thr Val Cys Asn
77   385                      390                      395                      400
78   Pro Val Gly Gly Asn Glu Lys Cys Ala Asp Val Thr Ile His Ile Phe
79           405                      410                      415
80   Phe Ser Lys Ile Leu Lys Leu Ala Ala Ile Arg Ile Arg Asn Leu Cys
81           420                      425                      430
82   Glu Arg Val Gln Cys Val Glu Gln Thr Glu Arg Val Tyr Asn Val Phe
83           435                      440                      445
84   Lys Gln Ile Leu Glu Gln Gln Thr Thr Leu Phe Phe Asn Arg His Ile
85           450                      455                      460
86   Asp Gln Leu Ile Leu Cys Cys Leu Tyr Gly Val Ala Lys Val Cys Gln
87   465                      470                      475                      480
88   Leu Glu Leu Thr Phe Arg Glu Ile Leu Asn Asn Tyr Lys Arg Glu Ala
89           485                      490                      495
90   Gln Cys Lys Pro Glu Val Phe Ser Ser Ile Tyr Ile Gly Ser Thr Asn
91           500                      505                      510
92   Arg Asn Gly Val Leu Val Ser Arg His Val Gly Ile Ile Thr Phe Tyr
93           515                      520                      525
94   Asn Glu Val Phe Val Pro Ala Lys Pro Phe Leu Val Ser Leu Ile
95   530                      535                      540
96   Ser Ser Gly Thr His Pro Glu Asp Lys Lys Asn Ala Ser Gly Gln Ile

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97      545      550      555      560
98      Pro Gly Ser Pro Lys Pro Ser Pro Phe Pro Asn Leu Pro Asp Met Ser
99              565      570      575
100     Pro Lys Lys Val Ser Ala Ser His Asn Val Tyr Val Ser Pro Leu Arg
101              580      585      590
102     Gln Thr Lys Leu Asp Leu Leu Leu Ser Pro Ser Ser Arg Ser Phe Tyr
103              595      600      605
104     Ala Cys Ile Gly Glu Gly Thr His Ala Tyr Gln Ser Pro Ser Lys Asp
105              610      615      620
106     Leu Ala Ala Ile Asn Ser Arg Leu Asn Tyr Asn Gly Arg Lys Val Asn
107     625      630      635      640
108     Ser Arg Leu Asn Phe Asp Met Val Ser Asp Ser Val Val Ala Gly Ser
109              645      650      655
110     Leu Gly Gln Ile Asn Gly Gly Ser Thr Ser Asp Pro Ala Ala Phe
111              660      665      670
112     Ser Pro Leu Ser Lys Lys Arg Glu Thr Asp Thr
113              675      680
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116 <211> LENGTH: 3747
117 <212> TYPE: DNA
118 <213> ORGANISM: Zea mays
119 <400> SEQUENCE: 2
120     gaattcggca cgagcaaagg tctgattgat atggaatggt tccagtcaaa tttggaaaaa 60
121     atggagaaac tatgtaattc taatagctgt aaaggggagc ttgattttta atcaattttg 120
122     atcaataatg attatatcc ctatgatgag aactcgacgg gggattccac caatttagga 180
123     cattcaaagt gtgcctttga aacattggca tctcccacaa agacaataaa gaacatgctg 240
124     actgttccta gttctccttt gtcaccagcc accggtgggt cagtcaagat tgtgcaaagt 300
125     acaccagtaa cttctgccat gacgacagct aagtggcttc gtgaggtgat atcttcattg 360
126     ccagataagc cttcatctaa gcttcagcag tttctgtcat catgcatag ggatttgaca 420
127     aatgctgtca cagaaagggt cagcatagtt ttggaagcaa tttttccaac caaatcttct 480
128     gccaatcggg gtgtatcgtt aggtctcaat tgtgcaaagt cctttgacat tccgtgggca 540
129     gaagccagaa aagtggaggc ttccaagttg tactataggg tattagaggc aatctgcaga 600
130     gcggagttac aaaacagcaa tgtaataaat ctaactccat tgctgtcaaa tgagcgtttc 660
131     caccgatggt tgattgcatg ttcagcggac ttagtattgg cgacacataa gacagtcatt 720
132     atgatgtttc ctgctgttct tgagagtacc ggtctaactg catttgattt gagcaaaaata 780
133     attgagaact ttgtgagaca tgaagagacc ctcccaagag aattgaaaag gcacctaaat 840
134     tccttagaag aacagctttt ggaaagcatg gcatgggaga aaggttcattc attgtataac 900
135     tcaactgattg ttgccaggcc atctgttgct tcagaaataa accgccttgg tcttttggct 960
136     gaaccaatgc catctcttga tgacttagtg tcaaggcaga atgttcgtat cgagggcttg 1020
137     cctgctacac catctaaaaa acgtgctgct ggtccagatg acaacgctga tctcgtatca 1080
138     ccaaagagat cgtgcaatga atctaggaac acagtagtag agcgcaattt gcagacacct 1140
139     ccaccaagc aaagccacat ggtgtcaact agtttgaaag caaaatgcc a tccactccag 1200
140     tccacatttg caagtccaac tgtctgtaat cctgttggtg ggaatgaaaa atgtgctgac 1260
141     gtgacaattc atatattctt ttccaagatt ctgaagttgg ctgctattag aataagaaac 1320
142     ttgtgcgaaa gggttcaatg tgtggaacag acagagcgtg tctataatgt cttcaagcag 1380
143     attcttgagc aacagacaac attatTTTTT aatagacaca tcgatcaact tatcctttgc 1440
144     tgtctttatg gtgttgcaaa ggtttgtcaa ttagaactca cattcaggga gatactcaac 1500
145     aattacaaaa gagaagcaca atgcaagcca gaagtttttt caagtatcta tattgggagt 1560
146     acgaaccgta atgggggtatt agtatcgcg ccatgttggtg tcattacttt ttacaatgag 1620

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147 gtatttgttc cagcagcgaa gcctttcctg gtgtcactaa tatcatctgg tactcatcca 1680
148 gaagacaaga agaattgctag tggccaaatt cctggatcac ccaagccatc tcctttccca 1740
149 aatttaccag atatgtcccc gaagaaagtt tcagcatctc ataattgtata tgtgtctcct 1800
150 ttgcggcaaa ccaagttgga tctactgctg tcaccaagtt ccaggagttt ttatgcatgc 1860
151 attggtgaag gcacccatgc ttatcagagc ccatctaagg atttggtgc tataaatagc 1920
152 cgcctaaatt ataattggcag gaaagtaaag agtcgattaa atttcgacat ggtgagtgac 1980
153 tcagtggtag ccggcagttc gggccagata aatgggtggt ctacctcgga tcctgcagct 2040
154 gcatttagcc ccctttcaaa gaagagagag acagatactt gatcaattat aaatggtggc 2100
155 ctctctcgta tatagctcac agatccgtgc tccgtagcag tctattcttc tgaataagtg 2160
156 gattaactgg agcgatttaa ctgtacatgt atgtgttagt gagaagcagc agtttttagg 2220
157 cagcaaactg tttcaagtta gcttttgagc tatcaccatt tctctgctga ttgaacatat 2280
158 ccgctgtgta gagtgttaat gaattcttag ttttcattgg gctgacataa caaatcttta 2340
159 tcctagttgg ctggttggtg ggaggcattc atcagggtta tatttggttg tcaaaaagta 2400
160 ctgtacttaa ttcacatctt tcacattttt cactagcaat agcagcccca aattgctttc 2460
161 ctgactagga acatattctt tacaggataa agcatgccaa ctctaaacta tatgaatcct 2520
162 ttttatattc tcatttttaa gtacttctct gtttctgcta cttttgtact gtatatttcc 2580
163 agcttctcca tcagactgat gatcccatat tcagtgtgct gcaagtgatt tgaccatatg 2640
164 tggcttatcc ttcagggtatg tctcatgttg tgacttcatt gctgattgct tttgtaatgg 2700
165 tactgttgag ttcatttctg gttacaatca gcctttactg ctttatattg ttctaactaa 2760
166 tttggcttgc acagccagga cgattgggtt tctgcatcaa tcaatctttt ttaggacaag 2820
167 atatttttgt atgtacact tcccaaattg caattaatcc agaagtctac cttgttttat 2880
168 tctattagtt ctcagcaaca gtgaatgaat atgaatcagt catgctgata gatgttcac 2940
169 tggttattcc aaacaatctg acatcgcatc tctttctgca agtgagatga agaaaacctg 3000
170 aaatgctatc accatttaaa acattggctt ctggaagttc aggtgattag caggagacgt 3060
171 tctgacattg ccattgacat gtacggtagt gatggcagga gacgttctta aacagcagct 3120
172 gctccttcag cttgtaattg ctgattgtat tgaccaagag catccacctt gccttatgg 3180
173 actaactgaa tgagctggtg acgctgactc atctgcataa tggcagatgc ttaaccatct 3240
174 ttaggagctc atgtcatgat tccagctgca ccgtgtcaaa tgtgaaggcc ctgcaaggct 3300
175 ttccaggccg caccaatcct gcttgcttct tgaagataca tatggtgcca cctaaataaa 3360
176 agctgtttct gggttatgtc gtccttgaca tgtcaacaga ttagtggttg gttgcagtca 3420
177 tgtggtgttt aagtcttgga gaaggcgaga agtcattgct gccagcattg tgatcgtcag 3480
178 gcacagaagt actcaaaagt gagagctact tgttgcgagc aaacggaggg cgatataggt 3540
179 tgatagccaa tttcagttct ctatatacaa gcagcggatt ttgttttagag ttagcttttg 3600
180 agatgcatca tttctttcac atctgattct gtgtgttgta actcggagtc gcgtagaagt 3660
181 tagaattgcta actgacctta attttcaccg aataatttgc tagcgttttt cagtatgaaa 3720
182 tccttgtctt aaaaaaaaaa aaaaaaa 3747

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184 <210> SEQ ID NO: 3

185 <211> LENGTH: 19

186 <212> TYPE: DNA

187 <213> ORGANISM: Artificial Sequence

188 <220> FEATURE:

189 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe

190 <400> SEQUENCE: 3

191 aatagacaca tcgatcaag

19

193 <210> SEQ ID NO: 4

194 <211> LENGTH: 18

195 <212> TYPE: DNA

196 <213> ORGANISM: Artificial Sequence

197 <220> FEATURE:

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198 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe
199 <400> SEQUENCE: 4
200     gtaatgatac caacatgg                                     18
202 <210> SEQ ID NO: 5
203 <211> LENGTH: 18
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
208 <400> SEQUENCE: 5
209     gatttaaaaat caagctcc                                     18
211 <210> SEQ ID NO: 6
212 <211> LENGTH: 199
213 <212> TYPE: PRT
214 <213> ORGANISM: Zea mays
215 <400> SEQUENCE: 6
216     Thr Pro Val Thr Ser Ala Met Thr Thr Ala Lys Trp Leu Arg Glu Val
217         1             5             10             15
218     Ile Ser Ser Leu Pro Asp Lys Pro Ser Ser Lys Leu Gln Gln Phe Leu
219         20             25             30
220     Ser Ser Cys Asp Arg Asp Leu Thr Asn Ala Val Thr Glu Arg Val Ser
221         35             40             45
222     Ile Val Leu Glu Ala Ile Phe Pro Thr Lys Ser Ser Ala Asn Arg Gly
223         50             55             60
224     Val Ser Leu Gly Leu Asn Cys Ala Asn Ala Phe Asp Ile Pro Trp Ala
225         65             70             75             80
226     Glu Ala Arg Lys Val Glu Ala Ser Lys Leu Tyr Tyr Arg Val Leu Glu
227         85             90             95
228     Ala Ile Cys Arg Ala Glu Leu Gln Asn Ser Asn Val Asn Asn Leu Thr
229         100            105            110
230     Pro Leu Leu Ser Asn Glu Arg Phe His Arg Cys Leu Ile Ala Cys Ser
231         115            120            125
232     Ala Asp Leu Val Leu Ala Thr His Lys Thr Val Ile Met Met Phe Pro
233         130            135            140
234     Ala Val Leu Glu Ser Thr Gly Leu Thr Ala Phe Asp Leu Ser Lys Ile
235         145            150            155            160
236     Ile Glu Asn Phe Val Arg His Glu Glu Thr Leu Pro Arg Glu Leu Lys
237         165            170            175
238     Arg His Leu Asn Ser Leu Glu Glu Gln Leu Leu Glu Ser Met Ala Trp
239         180            185            190
240     Glu Lys Gly Ser Ser Leu Tyr
241         195
243 <210> SEQ ID NO: 7
244 <211> LENGTH: 199
245 <212> TYPE: PRT
246 <213> ORGANISM: Xenopus sp.
247 <400> SEQUENCE: 7
248     Thr Pro Val Arg Gly Ala Met Asn Thr Val Gln Gln Leu Met Val Thr
249         1             5             10             15

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VERIFICATION SUMMARY

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